

#2 09/58 US-09-049-695-2.rst

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*****
*****
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Release 3.1A John F. Collins, Biocomputing Research Unit.
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Mpsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
run on: Tue Aug 3 18:01:42 1999; MasPar time 546.13 Seconds
1119.809 Million cell updates/sec
Tabular output not generated.

Title: >US-09-049-695-2
Description: (261) from US09049695.seq
Perfect Score: 261
N.A. Sequence: 1 AGCCACTGGAGCTCCTGAG.....GTCCAGAGCCGAACCTT 261
Comp:

Scoring table: TABLE default
Gap 5
Nmatch SID : Dbase 0; Query 0
Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

genbank-est11
gb_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1

Database:

gb_est11 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est20 20:gb_est20
21:gb_est21 22:gb_est22 23:gb_est23 24:gb_est24
25:gb_est25 26:gb_est26 27:gb_est27 28:gb_est28
29:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6
34:gb_est7 35:gb_est8 36:gb_est9 37:gb_gss1 38:gb_gss2
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description	Pred. No.
1	250	95.8	274	11	AA299977 EST11:2998 Uterus tumor I	1
2	241	92.3	378	19	T72043 Estrin	1
3	208	79.7	424	19	T78178 Ytgc3b05.r1	1
4	207	79.3	351	19	T85588 Soares rta	1
5	157	54.0	357	19	T86494 Yd81910.rl	1
C	5	150	51.3	531	14 AA502331 Soares feta	1
C	7	155	59.4	474	15 AA568450 ne55a10.s1 NCI_CGAP_CO	1
C	8	104	39.8	100	nm25b08.s1 NCI_CGAP_CO	1
9	100	38.3	550	26 A1391147 mcb5g01.y1	1	
10	100	38.3	590	25 A1323091 Soares mouse	1	

RESULT	LOCUS	DEFINITION	VERSION	REFERENCE	SOURCE	ORGANISM	ALIGMENTS
1	AA299977	274 bp mRNA	EST	gi:1952328 AA299977.1	EST.	Human.	vq3107.rl Barstead mo
						Homo sapiens	mb71h0.rl Soares mous
							ma46dl.rl Soares mous
							mb96e09.rl Soares mous
							mc3042.rl Soares mous
							ml15c06.rl Soares mous
							mb83g11.rl Soares mous
							mj73b05.rl Soares mous
							mb83h09.rl Soares mous
							mb44b07.rl Soares mous
							vt32h09.rl Barstead mo
							va47h04.rl Barstead bo
							vg42h10.rl Barstead bo
							vg34a08.rl Barstead bo
							mb29f05.rl Soares mous
							mb16g01.rl Soares mous
							ml85h09.rl Soares mous
							vgj3b08.rl Barstead bo
							mb74f08.rl Soares mous
							vg47a03.rl Barstead bo
							mb0378.rl Barstead bo
							9.92e-103
							4.92e-103
							8.94e-100
							6.67e-95
							2.03e-80
							8.94e-100
							6.82e-71
							2.15e-58
							8.91e-54
							vt32e02.rl Barstead mo
							9.78175459.rl Rice Immature
							mc07h12.rl Soares mous
							9.82e-39
							97SN1784 Rice Immature
							2.89e-37
							97SN1787 Rice Immature
							6.56e-33
							vgj36a07.rl Barstead bo
							97SN1784 Rice Immature
							4.89e-30
							ma400771.rl Soares mous
							mb89b1.rl Soares mous
							1.29e-28
							ou92f09.x1 NCI_CGAP_Ki
							4.82e-15
							AF038250 Human mRNA (T
							7.89e-10

On Sep 12, 1996 this sequence version replaced gi:1394394.

Other_ESIS: THCI04472
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3016599055
Fax: 3018699423
Email: akerlav@tigr.org
For clone availability, additional sequence and expression

Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 291
Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M1RPI
High quality sequence stop: 291.

FEATURES	Index (http://www.tigr.org/tgi/tgi/tgi.html)	Seq prime:	M13 Reverse
SOURCE		Location/Qualifiers	
		1. . 274	
		/organism="Homo sapiens"	
		/note="Organ: uterus; Vector: pBluescript SK-; Site_1:	
		EcoRI; Site_2: XbaI"	
		/db_Xref="NCBI (inhost):192971"	
		/db_Xref="taxon:606"	
		/clone lib="uterus tumor I"	
		/dev_stage="adult"	
BASE COUNT	60 a 80 c	84 g 46 t	4 others
ORIGIN			

```

Query Match      Score 250; DB 11; Length 274;
Best Local Similarity 95.8%; Pred No. 0.00e+00;
Matches 252; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```
BASE COUNT /lab_host="SOLR", cells_(kanamycin resistant)"  
          83 a 117 c 116 g 59 t 3 others  
ORIGIN
```

Db	1	CACTGAGCTCCCTGAGGACCTCTNTACAGAGAAGCAGCGGGACCCCAGACATGAGGGGGCTCT	50
QY	4	CACTGAGCTCCCTGAGCCTCTCTACAGAGCAGCGGGACCCCAGACATGAGGGGGCTCT	63
Ddb	61	CCTGGTCACCAAGCCTGGTGTGTCAGTCAGAGCAGCTGGGAGGAGCAGTGCTCCAGCACCAA	120
Qy	64	CCTGGTCACCAAGCCTGGTGTGTCAGTCAGAGCAGCTGGGAGGAGCAGTGCTCCAGCACCAA	123
Ddb	121	GSGTCCTATNAGATCAAGTNAACACTGGCTCTAGAGGAGGCCAGAGAGGCTG	180
Dy	124	GGTCCCTATCATCACAGATGCAAGTCAAACACTGGCCCTCTAGAGGAGGCCAGAGAAGGCTG	183
Db	181	GSGGCCCGTTGGGGAGCCTCCGGAGAAAGAACGAGCAGGAGTGGTGTGCTGTTCCCTGT	240
Dy	184	GSGGCCCGCTGGGGAGCCTCCGGAGAAAGAACGAGCAGGAGTGGTGTGCTGTTCCCTGT	240
Db	241	CCAGAAGCCGAACATT	258
Dy	244	CCAGAAGCCGAACCTT	261

RESULT FST 01 - MAP - 1995
FOCUS 2 T2043 378 bp mRNA

DEFINITION yc63005.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
 IMAGE: 65329 5', mRNA sequence.
 ACCESSION T72043
 NID 9686564
 VERSION T72043.1 GI:686654
 KEYWORDS EST.
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1
 (bases 1 to 378)
 AUTHORS Hillier,L., Clark,N., Dabuque,T., Ellioton,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Raskin,L., Rohlfing,T., Tan,F., Treviskis,E.,
 Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
 TITLE Wasil-Merck EST project
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314-266-1900

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 285 1800

Fax: 314 285 1810

Email: est@watson.wustl.edu

Insert Size: 644

High quality sequence stops: 403 Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: M13RP1

High quality sequence stop: 403.

FEATURES

Location/Qualifiers

source

1..424

/organism="Homo sapiens"

/note="Orgn: Liver and Spleen; vector: pRT3D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACGTGAGATTATAAGATCTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pRT3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.7%

Score 208;

DB 19;

Length 424;

Best Local Similarity

98.28%

Pred. No. 0.00e+00;

Matches 215;

Conservative

0;

Mismatches

3;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

0;

Mismatches

1;

Indels

1;

Gaps

1;

/db_xref="GDB:470059"

/clone="IMAGE:11452"

/clonelib="Soares fetal liver spleen INFSL"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

89 a 119 c 133 g 75 t 8 others

BASE COUNT

ORIGIN

Query Match

79.3%

Score 207;

DB 19;

Length 351;

Best Local Similarity

99.1%

Pred. No. 0.00e-00;

Matches 213;

Conservative

REFERENCE	AUTHORS	SOURCE	KEYWORDS
1	Hillier, L., Clark, N., Dubroque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.	Homo sapiens	Butcheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; 1 (bases 1 to 534)
TITLE	The WashU-Merck EST Project	IMAGE Consortium	NC-NCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL	unpublished (1995)	Washington University School of Medicine	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wuston.wustl.edu Insert Size: 716	Insert Length: 715 Seq primer: M13RPL High quality sequence stop: 232. Location/Qualifiers	Unpublished (1997) On Sep 12, 1996 this sequence version replaced gi:1407178.
FEATURES	source	1. .357/ <organism="Homo sapiens"> <note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACGCGAAGCTTATTAATTAAGCTTTTTTTTTTTT 3'], double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." /db_xref="txon:9606" <clone="IMAGE:14691"> <clone lib="Soares fetal liver spleen 1NFLS"> <dev_stage="20 week-post conception fetus"> <lab_host="DH10B (ampicillin resistant)"> BASE COUNT ORIGIN	Insert Length: 690 Std Error: 0.00 Seq primer: 40m13 fwd. ET from Amersham High quality sequence stop: 398. Location/Qualifiers
FEATURES	source	1. .534/ <organism="Homo sapiens"> <note="Vector: pRT3D-Pa (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) Primer. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization." /db_xref="taxon:9605" <clone="IMAGE:898523"> <clone lib="NCI-NCAP_Co3"> <sex="pooled"> <tissue type="colon"> <lab_host="DH10B">	Insert Length: 690 Std Error: 0.00 Seq primer: 40m13 fwd. ET from Amersham High quality sequence stop: 398. Location/Qualifiers
BASE COUNT	80 a 160 c 178 g 115 t 1 others	BASE COUNT ORIGIN	Insert Length: 690 Std Error: 0.00 Seq primer: 40m13 fwd. ET from Amersham High quality sequence stop: 398. Location/Qualifiers
FEATURES	source	1. .534/ <organism="Homo sapiens"> <note="Vector: pRT3D-Pa (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) Primer. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization." /db_xref="taxon:9605" <clone="IMAGE:898523"> <clone lib="NCI-NCAP_Co3"> <sex="pooled"> <tissue type="colon"> <lab_host="DH10B">	Insert Length: 690 Std Error: 0.00 Seq primer: 40m13 fwd. ET from Amersham High quality sequence stop: 398. Location/Qualifiers
RESULT	6	AA502331 DEFINITION ne26h06_s1 NCI_Co3 mRNA similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA	EST', human.
ACCESSION	AA502331	EST ID 92237299 VERSION AA502331.1 GI:2237298	EST', human.
RESULT	7	AA503839 DEFINITION ne5310.s1 NCI_Co3 mRNA similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA	EST', human.
LOCUS	501 bp	mRNA	EST', human.
DEFINITION	AA503839	mRNA	EST', human.
DEFINITION	ne5310.s1 NCI_Co3 mRNA	cDNA clone IMAGE:961050 3'	EST', human.
DEFINITION	similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA	IMAGE:961050 3'	EST', human.

ACCESSION	AA503839	NID	92341504
NID	g2238805	VERSION	AA568450.1
VERSION	g223839.1	KEYWORDS	EST.
KEYWORDS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	SOURCE	human.
SOURCE	Eutheria; Primates; Catarrhini; Hominidae; Homo.	ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 501)	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	AUTHORS	Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)	JOURNAL	Unpublished (1997)
COMMENT	On Apr 14, 1993 this sequence version replaced gi:693200.	COMMENT	On Sep 12, 1996 this sequence version replaced gi:1402127.
Contact:	Robert Strausberg, Ph.D.	Contact:	Robert Strausberg, Ph.D.
Tel:	(501) 496-1550	Tel:	(501) 496-1550
Email:	Robert_Strausberg@nih.gov	Email:	Robert_Strausberg@nih.gov
Tissue Procurement:	Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.	CDDNA Library Preparation:	M. Bento Soares, Ph.D.
CDNA Library Arrayed:	Greg Lennon, Ph.D.	DNA Sequencing:	Washington University Genome Sequencing Center
Clone distribution:	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html	Clone distribution:	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html
Insert length:	586 Std Error: 0.00	Insert length:	651 Std Error: 0.00
Seq primer:	-40ml3 fwd. ET from Amersham	Seq primer:	-40ml3 fwd. ET from Amersham
High quality sequence stop:	190.	High quality sequence stop:	197.
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
SOURCE	1. 5.01	SOURCE	1. 4.74
/organism="Homo sapiens"	/organism="Homo sapiens"	/organism="Homo sapiens"	/organism="Homo sapiens"
/note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded DNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. Library went through one round of normalization."	/note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded DNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."	/note="Organ: colon; Vector: PT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. Library was normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."	/note="Organ: colon; Vector: PT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. Library was normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."
BASE COUNT	62 a 148 c 165 g 126 t	BASE COUNT	61 a 142 c 157 g 114 t
ORIGIN		ORIGIN	
Query Match	59.4%	Query Match	39.8%
Best Local Similarity	98.1%	Score	155; DB 14; Length 501;
Matches	158; Conservative	Pred.	No. 3.4e-212;
Matches	0; Mismatches 3; Indels 0; Gaps 0;	Matches	104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	341 AAGAGTTCCGGCTCTGGACAGGAACGACCCAGCTGGTCCTCTCCGGAGCC 400	Db	371 AAGAGTTCCGGCTCTGGACAGGAACGACCCAGCTGGTCCTCTCCGGAGGC 430
Cp	261 AAGAGTTCCGGCTCTGGACAGGAACGACCCAGCTGGTCCTCTCCGGAGGC 202	Cp	261 AAGAGTTCCGGCTCTGGACAGGAACGACCCAGCTGGTCCTCTCCGGAGGC 202
Db	401 TCCACCAACGGGCCAGGTCTCTGGACAGGCTCTGGTCCTCTCCGGAGGC 460	Db	431 TCCACCAACGGGCCAGGTCTCTGGACAGGCTCTGGTCCTCTCCGGAGGC 474
Cp	201 TCCACCAACGGGCCAGGTCTCTGGACAGGCTCTGGTCCTCTCCGGAGGC 142	Cp	201 TCCACCAACGGGCCAGGTCTCTGGACAGGCTCTGGTCCTCTCCGGAGGC 153
Db	461 TGGATCTTGATAGGGACCTTGGCTCTGGACTCTGC 501	RESULT	9
Cp	141 TGCACTTGATAGGGACCTTGGCTCTGGACAGGCTCTGC 101	LOCUS	AI391147
RESULT	8	DEFINITION	560 bp mRNA
LOCUS	AA568450	EST	EST
DEFINITION	474 bp mRNA	09-SEP-1997	02-FEB-1999
	similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN .; mRNA		
ACCESSION	AA568450	KEYWORDS	proline-rich acidic protein (MOUSE); mRNA sequence.
ACCESSION	AI391147	NID	AI391147
VERSION	4217154	VERSION	4217154
KEYWORDS	EST	SOURCE	house mouse.
ORGANISM	Mus musculus	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

QY 222 ||||| | ||||| | ||||| | ||| | ||||| 255
 Db 163 AACAGGAACAGAGAAGGCTCAGGATACTAGAGCCCTGGAGGCCTTGAAAGGACACC 222
 QY 152 AGCAGGACCCAGAGAAGGCCCTGGGCCGGCTGGGAGGACGCC 221
 RESULT 11 W35494 578 bp mRNA EST 11-SEP-1996
 LOCUS mb71hi.0.1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
 DEFINITION IMAGE:334915 5', similar to gbj028486 Mus musculus uterine-specific
 proline-rich acidic protein (MOUSE); mRNA sequence.
 ACCESSION W35494
 NID 91318399
 VERSION W35494.1 GI:1318399
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 AUTHORS Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 578)
 JOURNAL Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubpuque,T.,
 COMMENT Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:215315
 Seq primer: ETPrimer
 High quality sequence stop: 401.
 FEATURES Source
 1. .578
 /organism="Mus musculus"
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 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTACCACTCTGAGTGGGAGCGGCCGATTTTTTTTTTT 3'],
 double stranded DNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 Dr. Minoru Ko (Wayne State University)."
 (db_xref="taxon:10090"
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 /clone.lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 BASE COUNT 143 a 155 c 159 g 114 t 7 others
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 Query Match 37.2%; Score 97; DB 34; Length 578;
 Best Local Similarity 73.8%; Pred. No. 1.55e-114;
 Matches 158; Conservative 0; Mismatches 55; Indels 1; Gaps 1;
 Db 44 CCCAGTCATGAGAGGTTCTCTGGCACCTCTGGCTGCGACAGCTGCTGGGAGG 103
 QY 42 CCCAGACATGAGGCTCTCTGGTGTGCTGGAGG 101
 Db 104 CAGGGCAGTC-AGCACACAGGCTCCGTCAAGCCAAGGAAACATGGTCCCTG 162
 QY 102 CAGGTGCACTCCAGCACCAAGGTCCTATCAAGATGCAAACACTGGCCCTCAG 161

QY 222 ||||| | ||||| | ||||| | ||| | ||||| 255
 Db 163 AACAGGAACAGAGAAGGCTCAGGATACTAGAGCCCTGGAGGCCTTGAAAGGACACC 222
 QY 152 AGCAGGACCCAGAGAAGGCCCTGGGCCGGCTGGGAGGACGCC 221
 RESULT 12 W10974 600 bp mRNA EST 01-OCT-1997
 LOCUS ma6d11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
 DEFINITION IMAGE:313749 5', mRNA sequence.
 ACCESSION W10974
 NID 91285279
 VERSION W10974.1 GI:1285279
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 AUTHORS Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 600)
 JOURNAL Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubpuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI: 204365
 Seq primer: ETPrimer
 High quality sequence stop: 477.
 FEATURES Source
 1. .600
 /organism="Mus musculus"
 /note="vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTACCACTCTGAGTGGGAGCGGCCGATTTTTTTTT 3'],
 double stranded DNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 Dr. Minoru Ko (Wayne State University)."
 (db_xref="taxon:10090"
 /map="21"
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 /clone.lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 BASE COUNT 165 a 161 c 155 g 119 t
 ORIGIN
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 Best Local Similarity 73.8%; Pred. No. 1.55e-114;
 Matches 158; Conservative 0; Mismatches 55; Indels 1; Gaps 1;
 Db 27 CCCAGTCATGAGAGGTTCTCTGGCACCTGTTGTGCTGGAGG 86
 QY 42 CCCAGACATGAGGCTCCCTGGTGTGCTGGAGG 101

ORIGIN

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/cclone="IMAGE:463594"
/cclone.lib="Soares mouse p3NMF19.5"
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Query Match Similarity 36.4%; Score 95; DB 34; Length 538;
 Best Local Similarity 73.4%; Pred. No. 3.20e-111;
 Matches 157; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Db 12 CCCAGTCATGAGGGTTCTCGGCCACCTGTGTTGGCTGCACTGCTGTGGAGG 71
 Qy 42 CCCAGACATGAGGGCTCTCTGGTACCAAGCAGCTGGTGTGCTGTGGAGG 101

Db 72 CAGGGCACCTC-ASCACACCAGGTCCTCTAACAGCAAACATGTGTCCTG 130
 Qy 102 CAGGTCAGTCAGCCAGCAAGGCTCATCAAGATGCGAGTCACACTGGCCCTAG 161

Db 131 AACAGGAACAGAGAGGGCTACTAGAGCCCTTGAAAGAAC 190
 Qy 152 AGCAGGACCCAGAGGAGGCCTGGGCCCTGGTGTGGAGGAGGAC 221

Db 191 AGCTGGGCCACTGTTCTGAAACCAACAGAA 224
 Qy 222 AGCTGGTGGCTGTCAGAAGCCAA 255

BASE COUNT

143 a 159 c 148 g 111 t

ORIGIN

ORIGIN

Query Match Similarity 36.4%; Score 95; DB 35; Length 557;
 Best Local Similarity 73.4%; Pred. No. 3.20e-111;
 Matches 157; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Db 21 CCCAGTCATGAGGGTTCTCGGCCACCTGTGTTGGCTGCACTGCTGTGGAGG 80
 Qy 42 CCCAGACATGAGGGCTCTCTGGTACCAAGCAGCTGGTGTGCTGTGGAGG 101

Db 81 CAGGGCACCTC-AGCACACCAGGTCCTCTAACAGCAAACATGTGTCCTG 139
 Qy 102 CAGGTCAGTCAGCCAGCAAGGCTCATCAAGATGCGAGTCACACTGGCCCTAG 161

Db 140 AACAGGAACAGAGAGGGCTACTAGAGCCCTTGAAAGAAC 199
 Qy 152 AGCAGGACCCAGAGGAGGCCTGGGCCCTGGTGTGGAGGAGGAC 221

RESULT 15

AK030782 557 bp mRNA EST 21-AUG-1996

DEFINITION m15c06_r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:453594

PROLINE-rich acidic protein (MOUSE);, mRNA sequence.

ACCESSION Ak030782

NID 91500770

VERSION Ak030782.1 GI:1500770

KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

RUELTERIA; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 557)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theisinger,B., Wyllie,I., Lennon,G., Soares,B., Wilson,R. and

Waterson,R.

TITLE The WashU-HMI Mouse EST Project

COMMENT Unpublished (1996)

On May 18, 1995 this sequence version replaced gi:811026.

Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 285 1800

Fax: 314 26 1800

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MG:277410 Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 459.

Location/Qualifiers

1. .557

/organism="Mus musculus"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5',

IGTRACCACTGAGGGAGGCCGGAATTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA was kindly provided by

Dr. Minoru Ko (Wayne State University). "

/db_xref="taxon:10090", " /db_xref="taxon:10090"



		/dev_stage="20 week-post conception fetus"
BASE COUNT	89 a 119 c	/lab_host="DH110B (ampicillin resistant)" 133 g 75 t 8 others
ORIGIN		
Query Match	49.7%	Score 309; DB 19; Length 424;
Best Local Similarity	92.0%	Pred. No. 0.00e+00; 0; Mismatches 23; Indels 11; Gaps 10;
Matches	390;	Conservative
Db	1	CCAGACATGAGGAGGTCTCTGGTCAACCGCTGTTGGTGTGCTGGAGGC
Oy	51	CCGAGACATGAGGAGGTCTCTGGTCAACCGCTGTTGGTGTGCTGGAGGC 60
Db	61	AGTGCACTCCAGCACCAAGTCCATCAAGTCAGTCAGTCAGTCAGTCAGCAACACTGGCCCTCAGA 120
Oy	111	AGGTGCACTCCAGCACCAAGTCCATCAAGTCAGTCAGTCAGTCAGCAACACTGGCCCTCAGA 170
Db	121	GCAGGAGCCAGGAAGGCTGG-CGCCGCTGGINGAGCTCCGGAGANGAGGACCA 179
Oy	171	GCAGGAGCCAGGAAGGCTGGGGCCGGCTGGAGGCTCCGGAGAAGGAGCACCA 230
Db	180	GCTGGNGTGTCTCTGAGAGCCGAACCTGTGACGACCGAGGAGGACAC 239
Oy	231	GCTGGTGTGCTGCTGTCAGAGGCCAACCTGTGACGACCGAGGAGGACAC 290
Db	240	AGGTCAAGGCAGGGGCCATTCCTCAGGGCACCAGGGCAGATGGAGGAGCAC 299
Oy	291	AGGTCAAGGCAGGGGCCATTCCTCAGGCACCAAGGCCATGGAGGAGCAC 350
Db	300	CCTGGGGCCGTCGCTGAGTCAGGAGCCATGAGCAGCAGTCACANCTNCGN 359
Oy	351	CCTGGG-CCTGTCCT-GAGT-CCGAGCCGACCATGACAGCCTG-ACCACTCCGC 406
Db	360	TGAGGAGGAACAGGGTCAAGGTAGAGGCCCTTGTGATGATNCAATTCAAC 419
Oy	407	TGAGGAGGA-CCAGG-CGAGG-AGAGGCCCGTGTGGGT-GAT-GCCAATCACC 460
Db	420	AGGT 423
Oy	461	AGGT 464
RESULT	5	
LOCUS	Aa503839	501 bp mRNA EST
DEFINITION	neu3a10_s1	NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:901050 3'
REFERENCE	92238806	similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN . , mRNA
VERSION	Aa503839.1	GI:2238806
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Etheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 501)	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	On Apr 14, 1993 this sequence version replaced gi:693200.	
Contact:	Robert Strausberg, Ph.D.	
Tel:	(301) 496-1550	
Email:	Robert_Strausberg@nih.gov	
M.D., Ph.D.	Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,	
CDNA Library Preparation: M. Bento Soares, Ph.D.		
CDNA Library Arraying: Greg Lennon, Ph.D.		
DNA Sequencing by: Washington University Genome Sequencing Center		
Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbrp/image/image.html		
RESULT	6	
LOCUS	T85589	457 bp mRNA EST
DEFINITION	Yd8g10_s1	Soares fetal liver spleen INFSL Homo sapiens cDNA clone
IMAGe	114786 3	, mRNA sequence.
ACCESSION	T85589	
NID	9713941	
VERSION	185589.1	GI:713941
KEYWORDS	EST.	

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 457)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Ellison,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffin,L., Rohlfing,T., Soares,M., Tan,F., Traskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	High quality sequence stops: 210 Source: IMAGE Consortium, INFLN This clone is available royalty-free through INFLN ; contact the IMAGE Consortium (info@image.infln.gov) for further information. Insert Length: 671 Std Error: 0.00 Seq primer: -21m13 High quality sequence stop: 210.
BASE COUNT	source 1. . 457 <i>/organism="Homo sapiens"</i> <i>/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5'-AAGCTTGGAAATTAAATTAAGAACCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."</i> <i>/db_xref="GDB:470403"</i> <i>/ab_xref="#" taxon:9605"</i> <i>/clone="IMAGE:114786"</i> <i>/sex="male"</i> <i>/dev_stage="20 week-post conception fetus"</i> <i>/lab_host="DH10B (ampicillin resistant)"</i> 73 a 121 c 146 g 106 t 11 others
ORIGIN	Query Match 48.6%; Score 302; DB 19; Length 457; Best Local Similarity 90.3%; Pred. No. 0.00e+00; Matches 400; Conservative 0; Mismatches 30; Indels 13; Gaps 13;
BASE COUNT	source 1. . 351 <i>/organism="Homo sapiens"</i> <i>/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5'-AAGCTTGGAAATTAAATTAAGAACCTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."</i> <i>/db_xref="GDB:470403"</i> <i>/ab_xref="#" taxon:9605"</i> <i>/clone="IMAGE:114786"</i> <i>/clone="IMAGE:114786"</i> <i>/sex="male"</i> <i>/dev_stage="20 week-post conception fetus"</i> <i>/lab_host="DH10B (ampicillin resistant)"</i> 76 a 100 c 107 g 64 t 4 others
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BASE COUNT	source 1. . 301 <i>/clone="IMAGE:114786"</i> <i>/clone="IMAGE:114786"</i> <i>/sex="male"</i> <i>/dev_stage="20 week-post conception fetus"</i> <i>/lab_host="DH10B (ampicillin resistant)"</i> 301
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BASE COUNT	source 1. . 5 <i>/clone="IMAGE:114786"</i> <i>/clone="IMAGE:114786"</i> <i>/sex="male"</i> <i>/dev_stage="20 week-post conception fetus"</i> <i>/lab_host="DH10B (ampicillin resistant)"</i> 5

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Best Local Similarity 97.5%; Pred. No. 0 00e-00; Mismatches 5; Indels 2; Gaps 2;

Matches 283; Conservative 0;

Qy 55 GCATGAGGAGGCTCCTGTGTCACAGCCAGCTGGTGTGCGGGAGGT 114
Db 65 GAGTCCCAGCCCCAAGTCTCATCAAGATGCAAGTCAGTCACACTGGCCCTCAGGCAG 124
Qy 115 GAGTCCAGCACCAAGGCTCTATCAAGATGCAAGTCAGTCACACTGGCCCTCAGGCAG 174
Db 125 GAGCCAGAGAACGCCCTGGGN-GCCCGTGGGGAGCTCCGGAGAGGAGGACAGCTG 183
Qy 175 GACCCAGAGAACGCCCTGGGGCCCGTGGAGGCTCCGGAGAGGAGGACAGCTG 234
Db 184 GGGTGTGTTCTGAGGAGGAACTCTGACCCAGGAGAACCCAGGT 243
Qy 235 GGGTGTGTTCTGAGGAGGAACTCTGACCCAGGAGAACCCAGGT 294
Db 244 CAGGGAGGGGCCCATCTTCAGGACCAGGGNTGGATGGAGAGGACCCACCTG 303
Qy 295 CAGGGAGGGGCCCATCTTCAGGACCAGGGNTGGATGGAGAGGACCCACCTG 354
Db 304 GGCTTTCTCTTAAGTCCNTAGCCGACCAT 335
Qy 355 GCGGCGTCTGAA-GTCCCG-AGCCGACCAT 384

RESULT 8 T72043 378 bp mRNA EST 01-MAR-1995
DEFINITION YC63b05_r1 Stratavene liver (#937224) Homo sapiens cDNA clone
IMAGE:83329 5', mRNA sequence.
ACCESSION T72043
VERSION T72043.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 378)
AUTHORS Hillier,L., Clark,N., Dubuge,T., Elliston,K., Hawkins,M.,
Holman,M., Ruffman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@atson.wustl.edu
High quality sequence stops: 291
Source: IMAGE Consortium LINL
This clone is available royalty free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 291.
FEATURES source
1. .378
/organism="Homo sapiens"
/note="Organ: liver; Vector: pBluescript SK; Site: 1:
/EcoRI; Site: 2: XbaI; Cloned unidirectionally. Primer:
Oligo dT. Hepatectomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACGAG 3', -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTT 3'"
/db_xref="GB:503386"
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/sex="male"
/age_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
BASE COUNT 83 a 117 c 116 g 59 t 3 others

RESULT 9 AA299977 274 bp mRNA EST 18-APR-1997
DEFINITION EST12598 Uterus tumor I Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA299977
VERSION AA299977.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 274)
AUTHORS Adams,M.D., Kerriavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirnstein,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghegan,N.S.,
Glodek,A., Gneim,C.L., Hana,M.C., Heedblom,E., Hinkle,P.S.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Matamoros,S.M., Merrick,J.M.,
Moreno-Palangues,R.F., McDonald,L.A., Noguyn,D.T., Pelliaggio,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,R.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hung,J., Li,H., Messner,P.S., Olsen,H.,
Raymond,L., Wet,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Bannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE JOURNAL MEDLINE
COMMENT On Sep 12, 1996 this sequence version replaced gi:1394394.
Other ESTs: Th104472
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 301699056
Fax: 301699423
Email: iarkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/db/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

42.8%

Score 265:

DB 11;

Length 274;

Best Local Similarity

97.8%;

Pred.

No.

0.00e+00;

Matches

268;

Conservative

0;

MisMatches

6;

Indels

0;

Gaps

0;

OY

Db

1

CACTGCAGAGCTCCCTGAGCAGCTCTTACAGAGACGGGACCCAGACATAGGAGGTCT

60

ACTGCAAGCTCTCTGAGACTCTACAGAGACGGGACCCAGACATAGGAGGTCT

71

CTGGTCACAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

12

ACTGCAAGCTCCCTGAGACTCTACAGAGACGGGACCCAGACATAGGAGGTCT

60

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72

OY

Db

61

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120

CTGGTCACAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

131

OY

Db

121

GGTCCCATNAAGATGCAAGTAAACACTGGCCCTCAGAGCAGGACCAAGAGCTG

180

GGTCCCATNAAGATGCAAGTAAACACTGGCCCTCAGAGCAGGACCAAGAGCTG

191

QY

Db

181

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251

QY

Db

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274

QY

Db

241

CTAGAAGCGGAACATTGACACACCGAGGAGGAG 285

QY

Db

252

CTAGAAGCGGAACATTGACACACCGAGGAGGAG 285

QY

RESULT

10

T86494

357

bp

mRNA

EST

17-MAR-1995

DEFINITION

y881h0.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone

IMAGE:146915', mRNA sequence.

ACCESSION

T86494

ND

ID

NID

VERSTON

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 357)

AUTHORS

Hillier,L., Clark,N., Dubuge,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikoff,L., Rohlfing,T., Soares,M., Tan,F., Treskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

COMMENT

Contact: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 285 1800

Fax: 314 285 1810

Email: est@wustl.edu

Insert Size: 716

High quality sequence stops: 232

Source: IMAGE Consortium, LNL

This clone is available royalty free through LNL; contact the

IMAGE Consortium (info.image.lnl.gov) for further information.

Insert length: 715

Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 232.

Location/Qualifiers

1. .357

source

FEATURES

source

Location/Qualifiers

42.8%

Score 265:

DB 11;

Length 274;

Best Local Similarity

97.8%;

Pred.

No.

0.00e+00;

Matches

268;

Conservative

0;

MisMatches

6;

Indels

0;

Gaps

0;

OY

Db

121

GGTCCCATNAAGATGCAAGTAAACACTGGCCCTCAGAGCAGGACCAAGAGCTG

180

GGTCCCATNAAGATGCAAGTAAACACTGGCCCTCAGAGCAGGACCAAGAGCTG

191

QY

Db

181

GGGGCCCCCTTGTTGAGGAGCTCGGCCCTCAGAGGAGGAGGACGACCTG

240

GGGGCCCCCTTGTTGAGGAGCTCGGCCCTCAGAGGAGGAGGACGACCTG

251

QY

Db

121

GAACAGGAGCTNGNGCCGNTGGGGAGGCTCCGGAGAAGGACGACCTG

180

GAACAGGAGCTNGNGCCGNTGGGGAGGCTCCGGAGAAGGACGACCTG

182

QY

Db

121

GAACAGGAGCTNGNGCCGNTGGGGAGGCTCCGGAGAAGGACGACCTG

238

QY

Db

181

TGCCTTCCCTGTCAGAGCCAACTCTGACCACGGAGAACCGACGGT

240

TGCCTTCCCTGTCAGAGCCAACTCTGACCACGGAGAACCGACGGT

284

QY

Db

241

GCAGGGCCCCATCCTTCCAGG-CACCAAAGGCCCTGGATGGAGA

340

QY

RESULT

11

AA335186

188

bp

mRNA

EST

21-APR-1997

DEFINITION

EST3964

Epididymus

Homo sapiens

cDNA

5' end

mRNA sequence.

ACCESSION

91987501

ID

AA335186.1

GI:1987501

VERSION

AA335186.1

EST.

KEYWORDS

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 188)

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulmer,R.A.,

Bult,C.J., Deo,N.H., Kirkness,E.F., Weinstock,K.G., Goedeyne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., May-Wai,C., Fine,L.D.,

Clayton,R.A., Cline,T.R., Cotton,D., Earle,Hughes,J., Fine,L.D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hebliden,E., Hinkle,P.S.Jr.,

Kelly,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merri,J.M.,

Moreno-Palangue,R.F., McDonald,L.A., Nguyen,D.T., Peilgrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weddman,J., Li,Y.,

Bednarik,D.P., Gao,L., Celeda,M.A., Coleman,T.A., Collins,E.J.,

Dunke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,

He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak,D.L., Kunisch,C., HungJung,J., Li,H., Meissner,P.S., Oles,H.,

Raymond,L., Wei,Y.F., Wing,J.J., Xu,C., Yu,G.L., Ruben,S.M.,

Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,

FEATURES

source

Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Ehnmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arranging: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution by: NCT-CGAP clone distribution information can be
found through the T. M. G. E. Consortium/LINL at:
www-tig.tigr.org/EBI/mars/mars.html

Trace considered overall poor quality
Insert Length: 547 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

Location/Qualifiers
1.. 139
organism="Homo sapiens"
/note "vector: pRTD-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."
.

COMMENT

On Apr 14, 1993 this sequence version replaced gi:716750.

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 285 1810

Email: mouseest@wustl.edu

This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 486.

FEATURES

source

Location/Qualifiers

1..550

/organism="Mus musculus"

/note="vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAGTGCGGGCCATTTCCTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia).

Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

/db_xref="taxon:10090"
/map="12"

/clone="IMAGE:348720"

/clone.lib="Soares mouse P3NMF19.5"
/lab_host="DH10B (ampicillin resistant)"

BASE COUNT

136 a 162 c 148 g 113 t 1 others

ORIGIN

Query Match

16.6%; Score 103; DB 26; Length 560:

Best Local Similarity 71.7%; Pred. No. 4.21e-122;

Matches 170; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 44 CCCAGTCATGAAAGGTTCTCCGGCACCTGTTGGCTGCACGTGCTGGAGG 103
Qy 50 CCCAGACATGAGGAGGCCTCTCTGGTACACAGCCTGGTGTGCTGTGGAGG 109

Db 104 CAGGGCAGCTCCACACAGGTCCTCTCAAGCAGGAACATGTTCCCTG 163
Qy 110 CAGGGCAGCTCCACCAAGGCCCTATCAAGTGAAGTCAACACTGGCTCAG 169

Db 154 AACAGAAACAGAGAGGGCTGGATACTAGAGCCCTGGCTTGAAAGAAC 223
Qy 170 AGCAAGACCCAGAGGAGGGCCCTGGTGGAGGACCTCCGGAGAGGAC 229

Db 224 AGCTGGGCCACTGCTCTGAACCAAAGAGAACCTGCGAGCTGCCGAGGAAGC 280
Qy 230 AGCTGGGGCTGTCCTCCCTGTCAGAACGCGAACCTGACCAACCGAGGAAGC 286

RESULT 14 AT323091 590 bp mRNA EST 23-DEC-1998

DEFINITION mb73b06.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:817155, similar to gb:U08486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION A1323091
NID 64057520
VERSION At323091.1
KEYWORDS EST.
SOURCE house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
1 (bases 1 to 590)

REFERENCE

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE

The WashU-HMM Mouse EST Project

JOURNAL

Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:693536.

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

McI:92459
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco

FEATURES

source

Location/Qualifiers

1..590

/organism="Mus musculus"

/note="vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAGTGCGGGACGGCCATTTCCTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia).

Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

/db_xref="taxon:10090"

/map="12"

/clone="IMAGE:481715"

/clone.lib="Soares mouse P3NMF19.5"

/lab_host="DH10B (ampicillin resistant)"

BASE COUNT

152 a 167 c 151 g 118 t 2 others

ORIGIN

Query Match

16.6%; Score 103; DB 25; Length 590:

Best Local Similarity 71.7%; Pred. No. 4.21e-122;
Matches 170; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 46 CCCAGTCATGAGGGTTCTCTGGCTCACCGCTTGTGCTGAGC 105
Qy 50 CCCAGACATGAGGGCTCTCTGGTACACGCCTGTTGGTGTGGCTGGAGG 109

Db 106 CAGGGCAGCTCCAGCACCAAGGCTCCCTGTCAGACAGAACATGIGTCCC 165
Qy 110 CAGGGCAGCTCCAGCACCAAGGCTCCATCAAGTGAAGTCAACACTGGCTCAG 169

Db 165 AACAGAAACAGAGAGGGCTGGAGATAAGACCTGCTGAGCCCTGAGAACAC 225
Qy 170 AGCAGGACCCAGAGAGGCCTGGGGCGCCGTTGGAGGACCTCCGGAGGAC 229

Db 226 AGCAGGGCCACTGCTCTGAACCAAAGAGAACCTGCGAGCTGCAGTGCC 282
Qy 230 AGCTGGGGCTGTCCTCCCTGTCAGAACGCGAACCTGACCAACACTGGCTCAG 286

RESULT 15 W36494 578 bp mRNA EST 11-SEP-1996

DEFINITION mb71h0.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:334915, similar to gb:U028486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE), mRNA sequence.

Search completed: Tue Aug 3 20:36:22 1999
Job time : 1507 secs.

ACCESSION W36494
NID 91318399
VERSION W36494.1 GI:1318399
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Buteraria; Rodentia; Sciuromyath; Muridae; Murinae; Mus.
AUTHORS Marra,M., (bases 1 to 578), Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubroque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU HHMI Mouse EST Project
COMMENT Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430545.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This Clone is available royalty-free through LInL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:216315
Seq primer: Empriem
High quality sequence stop: 401.

FEATURES source
 /organism="Mus musculus"
 /note="vector: pR73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dt) primer [5',
 TGTATCCAACTTGAGTGGGCGCATTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pR73 vector
 (Pharmacia). Library went through one round of
 normalization to a COT = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 /db_xref="taxon:10090"
 /map="21"
 /clone="IMAGE_334915"
 /clone_id="Soares mouse P3NNF19_5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 BASE COUNT
 ORIGIN
 Query Match 16.18; Score 100; DB 34; Length 578;
 Best Local Similarity 72.2%; pred. No. 3 85e-117; Gaps 1;
 Matches 171; Conservative 0; Mismatches 65; Indels 1; Gaps 1;
 Db 44 CCCAGTCATGAGAGGTCTCTCTGGGCCACCTGGTGGTGGCACTGCTGGGAGG 103
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 50 CCCAGACATGAGGGAGCTCTCCCTGGTCACCAAGCAAAACTGTTCCCTG 109
 Db 104 CAGCGGACTCC-NGCACACCAGGCTCCCTGCAAGACCAAGAACATGTTCCCTG 162
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 110 CAGTGCACTCCACGACCCAAGGCTCTATCAGATGCAACTGCCCCCTAG 169
 Db 163 AACGGAAACAGAGGAGGTCTGAGATACTAGAGCTCTGGACCTTCAAAGACACC 222
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 170 AGGAGGACGCCAGGAAGGCCTGGGCCCGTGTGGAGCCTCCGGAGAAGGACGACC 229
 Db 223 AGCTGGGCCACTCTCTGAAACAGAGGAGCTGCGAGGAGAAAG 279
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 230 AGCTGGGCCACTCTGAAACAGAGGAGCTGCGAGGAGAAAG 286

Page 1

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

Title: >US-09-049-695-1
Description: (1-254) from US09049695.seq
Perfect Score: 254

Nmatch SID : Dbase 0: Query 0
searched: >8813791 secs 117158079 bases x?

Post-processing: Minimum Match 0%
Listing first 45 summaries

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13:gb.est14 14:gb.est15 15:gb.est16 16:gb.est17  
17:gb.est18 18:gb.est19 19:gb.est20 20:gb.est20  
21:gb.est21 22:gb.est22 23:gb.est23 24:gb.est24  
25:gb.est25 26:gb.est26 27:gb.est27 28:gb.est28
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23:gb_gss3 30:gb_gss3 31:gb_gss3 32:gb_gss3 33:gb_gss3 34:gb_gss3 35:gb_gss3 36:gb_gss3 37:gb_gss1 38:gb_gss2
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

```

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Resilient
Organizations
SUMMARIES

NO.	SYNTHETIC NUCLEOTIDE	SEQUENCE	LOCATION	REF.
1	237	93-11	274-11	RA299977
	228	89-8	378-19	EST12598 Uterus tumor Yc63005.r1 Stratagene 0.00e+00

4									
5	192	75.6	351	19	T855498	Yd8910.rl	Scores	feta	1.57e-272
5	152	59.7	357	19	A50331	NCl-GAP-Co	1.2e-192		
5	145	57.1	534	14	A503815	ne53110	NCI-GAP-Co	2.e-14	
5	55	57.1	501	14					

8	39.0	56.0	21391147	mc16901.YI	Soares	mous	2.44e-116
9	39.0	56.0	213920392	mb7110.11	Soares	mous	1.84e-111
9	37.3	57.8	W56494				

ALIGNMENT

C	11	96	37.8	600	33	W10974	ma6dd11.r1 Soares mouse	1.84e-11
C	12	96	37.8	1114	34	W29238	mb96109.r1 Soares mouse	1.84e-11
C	13	94	37.0	557	35	AA030782	mc22019.r1 Soares mouse	3.23e-10
C	14	94	37.0	565	34	W36411	mb81911.r1 Soares mouse	3.23e-10
C	15	94	37.0	571	35	AA020553	mj73206.r1 Soares mouse	3.23e-10
C	16	94	36.2	418	35	AA020553	mb6109.r1 Soares mouse	5.56e-10
C	17	92	36.2	431	35	W08257	mb44b07.r1 Soares mouse	5.56e-10
C	18	92	36.2	478	17	AA691263	vt32109.r1 Barstead bo	5.56e-10
C	19	92	36.2	510	20	AA871980	vq7704.r1 Barstead bo	5.56e-10
C	20	92	36.0	474	15	AA580935	nn2tb08.r1 NCLCGAP bo	3.83e-10
C	21	89	35.0	508	20	AA871942	vnq42110.r1 Barstead bo	3.83e-10
C	22	89	35.0	572	20	AA871332	vq3408.r1 Barstead bo	3.83e-10
C	23	89	35.0	379	33	W14887	mb29105.r1 Soares mouse	6.29e-07
C	24	87	34.3	379	33	W14887	mb83103.r1 Soares mouse	6.29e-07
C	25	87	34.3	477	33	W17866	mj68505.r1 Soares mouse	6.29e-07
C	26	87	34.3	543	35	AA060592	vq3208.r1 Barstead bo	6.29e-07
C	27	87	34.3	586	35	AA871263	mb74108.r1 Soares mouse	1.01e-03
C	28	85	33.5	463	33	W17574	vnq44110.r1 Barstead bo	4.02e-02
C	29	84	33.1	498	20	AA87078	mc21001.r1 Soares mouse	2.04e-02
C	30	76	29.9	323	30	W20635	mi185109.r1 Soares mouse	5.21e-02
C	31	70	27.6	212	33	AA038591	SSCI09B05 Porcine small	1.15e-01
C	32	62	24.4	366	20	F230350	vq51608.r1 Barstead mo	1.65e-01
C	33	58	22.4	485	16	AA64747	vt3202.r1 Barstead mo	4.37e-02
C	34	57	22.4	534	16	AA690880	mc01712.r1 Soares mouse	3.04e-02
C	35	49	19.3	540	34	W29238	mc01712.r1 Soares mouse	3.04e-02
C	36	47	18.5	252	17	AA754549	97SN1787 Rice Immature	2.39e-35
C	37	45	17.7	247	17	AA754458	97SN1784 Rice Immature	1.75e-32
C	38	45	17.7	252	17	AA754549	97SN1787 Rice Immature	1.75e-32
C	39	45	17.3	247	17	AA754548	97SN1784 Rice Immature	4.61e-31
C	40	44	17.3	456	20	AA871185	vq36807.r1 Barstead bo	4.61e-31
C	41	43	16.9	479	33	W10393	mb89111.r1 Soares mouse	1.19e-01
C	42	42	16.5	100	33	AF038250	mb89111.r1 Soares mouse	6.99e-02
C	43	41	11.0	1287	20	AF038250	Human mRNA (T)	1.08e-05
C	44	27	10.6	302	16	AA522167	nq541012.s1 NCLCGAP co	1.08e-08
C	45	27	10.6	227	16	AF03473	Human mRNA (T)	1.08e-08

Other_ESTs: THC104472

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 301869056

Fax: 301869423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

FEATURES

Seq primer: M13 Reverse

Location/Qualifiers

1. .274

/organism="Homo sapiens"

/note="Organ: uterus; Vector: pBluescript SK-; Site_1:

/db_xref="NCBI (inhost):192971"

/db_xref="taxon:9606"

/clone.lib="uterus tumor I"

/dev_stage="adult"

/80 c 84 g 46 t 4 others

BASE COUNT

60 a

80 c

84 g

46 t

4 others

ORIGIN

Query Match

Best Local Similarity 93.3%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

1 CACTGAGCTCCCTGAGCACTCTNTACAGAGACGGGACCCCACATAGGGAGCTCT

/note="Organ: uterus; Vector: pBluescript SK-; Site_1:

/db_xref="NCBI (inhost):192971"

/clone.lib="uterus tumor I"

/dev_stage="adult"

/80 c 84 g 46 t 4 others

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="IMAGE:85329"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

3 others

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

12 CACTGAGCTCCCTGAGCACTCTNTACAGAGACGGGACCCCACATAGGGAGCTCT

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

Fax: 314 286 1810

Email: estwattson.wustl.edu

High quality sequence stop: 291

Source: IMAGE Consortium, LNL

This Clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: M13RPL

High quality sequence stop: 291.

Location/Qualifiers

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.2%

Score 228; DB 19; Length 378;

Matches 244; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Db

7 GAGCAGCCACTCTAAGCTCCCTGAGACCTCTACAGAGACCGGGACCCAGACATGAGG

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

132 GGTCCTATCAACATGCAACTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

181 GCGCCGCGTTGGTGGAGCTCGCTGGAGAACAGGAGCAGCTGCTGCTGCTGCTG

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

192 GGCGCCGCGTTGGTGGAGCTCGCTGGAGAACAGGAGCAGCTGCTGCTGCTGCTG

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

241 CCA 243

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

252 CCA 254

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

59 t

ORIGIN

Query Match

Best Local Similarity 97.9%

Score 237; DB 11; Length 274;

Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db

253 CCA 255

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

FEATURES

Source

1. .378

/organism="Homo sapiens"

/note="Organ: liver; Vector: pBluescript SK-; Site_1:

/db_xref="GDB:50286"

/clone.lib="Stratagene liver (#937224)"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT

83 a

117 c

116 g

5

REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikitin, L., Ronning, T., Soares, M., Tan, F., Trevakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

INSERT SIZE: 716
High quality sequence stops: 232 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

SEQ PRIMER: M13RP1
High quality sequence stop: 232.

FEATURES
SOURCE
I. .357

/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: PT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACIGGAGATTAATGATCTTTTCTTTTCTTTT3'], double-stranded cDNA was ligated with Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified PT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="GDB:470308"
/db_xref="taxon:9006"
/clone="IMAGE:114691"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
ORIGIN
72 a
101 c 112 g 64 t 8 others

BASE COUNT
Query Match 59.8%; Score 152; DB 19; Length 357;
Best Local Similarity 94.4%; Pred. No. 1.76e-204; Indels 0; Mismatches 185; Conservative 0; Gaps 4;

1 AGGCCTCCCTGCACGCCAGCCTGGTGTGCTGCTGCGAGGCCAGTCAGTCCC 60
64 AGGCCTCCCTCCTGGTCACAGGCCAGCTGGT-TGGCTGCTGTTGGAGSGAGTCAGTCAGRCCC 122

Db 61 AGCACCCAAAGGCTCTAAGTCAAGSTGCAAGTCAAACACTGGCCCTCAGCACGAGCCAGA 120
123 AGCACCCAAGGCTCTAAGTCAAGTCAACTGGCCCTCAGCACGAGCCAGA 182

Qy 121 GAACAGGCCTINGNGCCGTGTTGGGGACCTCGGAGAGGACGAGCTGTG 180
Qy 183 GAA-GGCGTGGGSCCGT-GTGG-TGGACCTCGGGAGAGGAGGACGAGCTGTG 238

Db 181 TGCGTGTCCCTGTC 196
Qy 239 TGCTGTCCCTGTC 254

RESULT 5
LOCUS AA502331 534 bp mRNA EST 19-AUG-1997
DEFINITION ne56h06_s1 NCBI CGAP_Co3 Homo sapiens cDNA clone IMAGE:898523 3'
SIMILAR TO TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA sequence.

ACCESSION AA502331
NID 923805
VERSION AA503839.1
EST GI:2238806

REFERENCE
AUTHORS Eutheria: Primates: Catarrhini; Hominoidea; Homo.
ORGANISM Homo sapiens
SOURCE human.
COMMENT

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 435-1550
Email: Robert_Strausberg@nih.gov

Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center found through the T.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 690 Std Error: 0.00
Seq Primer: -40m13 fwd. ET from Amersham

FEATURES
SOURCE
I. .534

/organism="Homo sapiens"
/note="Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT7T3 vector. Library went through one round of normalization."
/db_xref="taxon:9606"
/clone="IMAGE:98523"
/clone_lib="NCI-CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
ORIGIN
80 a
160 c 178 g 115 t 1 others

BASE COUNT
Query Match 57.1%; Score 145; DB 14; Length 534;
Best Local Similarity 94.6%; Pred. No. 1.12e-192; Indels 0; Mismatches 158; Conservative 0; Gaps 1; Gaps 1;

Db 369 TTGACAGGGACAGCACACAGCTGGTCTCTCTCCGAGGTCCACACGGGG 428
254 TGGACAGGGACAGCACACAGCTGGTCTCTCTCCGAGGTCCACACGGGG 195

Cp 429 CCCAGGC-TTCCTGGTCTGCTCTGGAGGAGGTGTTGACTTGCACTTGATAGG 487
Cp 194 CCCAGGC-TTCCTGGTCTGCTCTGGAGGAGGTGTTGACTTGCACTTGATAGG 135

Db 488 ACTGGGGCTGGGAATGGACCTGGCTCCACAGAGAAACAC 534
Cp 134 ACCTGGGGCTGGGAATGGACCTGGCTCCACAGAGAAACAC 88

RESULT 7
LOCUS AA503839 501 bp mRNA EST 19-AUG-1997
DEFINITION ne53a10_s1 NCBI CGAP_Co3 Homo sapiens cDNA clone IMAGE:901050 3'
SIMILAR TO TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA sequence.

ACCESSION AA503839
NID 923805
VERSION AA503839.1
EST GI:2238806

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 501)
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T.,
 NCI-CGAP (<http://www.ncbi.nlm.nih.gov/ncicgap>).
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL On Apr 14, 1993 this sequence version replaced gi:593200.

COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov

Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the L.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 586 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 190.

FEATURES SOURCE
 Location/Qualifiers

1. .501

/organism="Homo sapiens"

/note="Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; site 2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization." /db_xref="taxon:9606"
 /clone="IMAGE:901050"
 /clone_lib="NCI_CGAP_Co3"
 /sex="pooled"
 /tissue,type="colon",
 /lab_host="DH10B"

BASE COUNT
 ORIGIN
 Query Match 55.1%; Score 140; DB 14; Length 501;
 Best Local Similarity 97.9%; Pred. No. 2.84e-184;
 Matches 143; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 355 TGGACAGGAAACGACCCAGCTGGTCCTCTCCGGAGGCCTCACCCACGGGG 415
 Cp 254 TGGACAGGAAACGACCCAGCTGGTCCTCTCCGGAGGCCTCACCCACGGGG 195

Db 415 CCCAGGTCTCTGGGCCCTGAGGCCAGTGTTGACTTGATCTGTAGGG 475
 Cp 194 CCCCAAGCCTCTGGCTCTGAGGCCAGTGTTGACTTGATCTGTAGGG 135

Db 476 ACCTGGGIGGGAGCTGACTGG 501
 Cp 134 ACCITGGGTGGGACTGACCTGC 109

FEATURES SOURCE
 Location/Qualifiers

1. .560

/organism="Mus musculus"

/note="Vector: pMT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTRACCACTGCTGAGGGAGGGCATTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pMT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)." /db_xref="taxon:10090"
 /map="12"
 /clone="IMAGE:348720"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"

BASE COUNT
 ORIGIN
 Query Match 39.0%; Score 99; DB 25; Length 560;
 Best Local Similarity 74.6%; Pred. No. 2.44e-116;
 Matches 150; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 44 CCCACATGAGGGCTCTGGTCACCCGCTGGTGGCATCTGGGG 103
 Qy 50 CCCAGACATGAGGGCTCTGGTCACCCGCTGGTGGCATCTGGGG 109

Db 104 CAGGGCAGSTCCACACCCAGGCTCTGCAAGACCAAAGAACATGTCCTCG 163

Qy 110 CAGGGCAGSTCCACACCCAGGCTCTGCAAGACCAAAGAACATGTCCTCG 169

Db 164 AACAGAAACAGAGAAGCTGGGACTAGAGCCCTTGAAAGAACAC 223

Qy 170 AGCAGAAACAGAGAAGCTGGGACTAGAGCCCTTGAAAGAACAC 229

FEATURES SOURCE
 Location/Qualifiers

RESULT 8 AI391147 560 bp mRNA EST 02-FEB-1999

DEFINITION m15901.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:348720, similar to gb:U22486 Mus musculus uterine-specific prolipoprotein-rich acidic protein (MOUSE);, mRNA sequence.

ACCESSION A1361147
 VERSION 94217154
 EST. A191147.1 GI:4211154

SOURCE house mouse.

FEATURES SOURCE
 Location/Qualifiers

RESULT 9 AI323091 590 bp mRNA EST 23-DEC-1998

DEFINITION mJ3b06.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone

IMAGE:481715 5' similar to gb:U28486 Mus musculus uterine-specific

ACCESSION

NID

VERSION

KWORDS

EST.

house mouse.

Mus musculus

ORGANISM

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 590)

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RESULT 11 Locus w10974 600 bp mRNA EST 01-OCT-1997
 Definition ma46d11.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
 Accession W10974
 NID 91285279
 Version V10974.1 GI:1285279
 Keywords EST.
 Source house mouse.
 Organism Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Reference 1 (bases 1 to 600)
 Authors Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 Title The WashU-HMMI Mouse EST Project
 Journal Unpublished (1996)
 Comment Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 285 1800
 Fax: 314 285 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI: 204365
 Seq primer: ETPrimer
 High quality sequence stop: 477.
 Location/Qualifiers
 FEATURES
 Source
 /organism="Mus musculus"
 /note="Vector: pT7T3 (Pharmacia) with a modified
 polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA
 was primed with a Not I - Oligo(dT) primer [5',
 TGTATCCATCTGAAAGGGGACGCCGATTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 /db_xref="taxon:10090"
 /clone="IMAGE:313749"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 BASE COUNT 165 a 151 c 155 g 119 t
 ORIGIN
 Query Match 37.8%; Score 96; DB 33; length 500;
 Best Local Similarity 75.1%; Pred. No. 1.84e-11; Mismatches 151; Conservative 0; Indels 1; Gaps 1;
 DB 27 CCCAGTCATGAGAGGTCTCTGGCACCGTTCGACTGCTGGAG
 BASE COUNT 245 a 217 c 420 g 215 t 17 others
 ORIGIN
 Query Match 37.8%; Score 96; DB 34; Length 114;

RESULT 12 Locus w29238 1114 bp mRNA EST 11-SPP-1996
 Definition mb96e9.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
 Accession W29238
 NID 91309520
 Version V29238.1 GI:1309520
 Keywords EST.
 Source house mouse.
 Organism Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Reference 1 (bases 1 to 1114)
 Authors Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 Title The WashU-HMMI Mouse EST Project
 Journal Unpublished (1996)
 Comment On Apr 14, 1993, this sequence version replaced gi:785474.
 Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:248688
 Seq primer: ETPrimer
 High quality sequence stop: 388.
 Location/Qualifiers
 FEATURES
 Source
 /organism="Mus musculus"
 /note="Vector: pT7T3 (Pharmacia) with a modified
 polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA
 was primed with a Not I - Oligo(dT) primer [5',
 TGTATCCATCTGAAAGGGGACGCCGATTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia) digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 /db_xref="taxon:10090"
 /clone="IMAGE:337288"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 BASE COUNT 245 a 217 c 420 g 215 t 17 others
 ORIGIN
 Query Match 37.8%; Score 96; DB 34; Length 114;

QY 110 CAGCTGCAGTCCCCAGCACCAAGGCTCTATCAAGATGCAAGTCAGACTGCCCCCTCAG 169
 Db 153 AACAGGAACAGGAAGGTCTGGATACTAGAAGCCCTTGAGGAAAGACAACC 222
 QY 170 AGCAGGACCCAGAGAAGGGCTGGGCCGCGCTGGTGGAGGAGAACCC 229
 Db 223 AGCTGGGCCACTCTCTCTG 243
 QY 230 AGCTGGTGGCTGCTCCCTG 250

QY 50 CCCAGACATGAGGAGGCCTCTCTGGTACCGCCCTGGTGTGCTGCTGGAGG 109
 Db 87 CAGCGCGAGTCC-AGCACACAGGCTCTGTGAGACCAAGCAAGATGTTCTG 145
 QY 110 CAGCTGCAGTCCCCAGCACCAAGGCTCTATCAAGATGCAAGTCAGACTGCCCCCTCAG 169
 Db 145 AACAGGAACAGAGAAGGTCTGGATACTAGAAGCCCTTGAGGAAAGACACC 205
 QY 170 AGCAGGACCCAGAGAAGGGCTGGGCCGCTGGTGGAGGAGAACCC 229

Best Local Similarity 75.1%; Pred. No. 1.84e-11; Matches 151; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

DEFINITION mc25c10_r1 Soares mouse p3NME19.5 Mus musculus EST mRNA clone
IMAGE:349554 5' similar to qb:U28486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION W30342
VERSION NID 91310492
KEYWORDS EST
ORGANISM Mus musculus
SOURCE house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,N.
TITLE Unpublished (1995)
JOURNAL On Apr 14, 1995 this sequence version replaced gi:838193.
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:221354
Seq Primer: ET-Primer
High quality sequence stop: 423.

FEATURES source
1. .538
/organism="Mus musculus"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TCTTACCAACTGTAAGTGGGAGGCCGCCTTTTTTTTTT 3'], double stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minru Ko (Wayne State University)." /clone="IMAGE:349554" /clone_id="Soares mouse p3NME19.5" /dev_stage="19.5 dpc total fetus,"

RESULT 13
DEFINITION W30342 538 bp mRNA
IMAGE:349554 5' similar to qb:U28486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION NID 91310492
VERSION VERSION EST
KEYWORDS EST
ORGANISM Mus musculus
SOURCE house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,N.
TITLE Unpublished (1995)
JOURNAL On Apr 14, 1995 this sequence version replaced gi:838193.
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:221354
Seq Primer: ET-Primer
High quality sequence stop: 423.

FEATURES source
1. .538
/organism="Mus musculus"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TCTTACCAACTGTAAGTGGGAGGCCGCCTTTTTTTT 3'], double stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minru Ko (Wayne State University)." /clone="IMAGE:349554" /clone_id="Soares mouse p3NME19.5" /dev_stage="19.5 dpc total fetus,"

BASE COUNT 131 a /lab host="DH10B (ampicillin resistant)"
ORIGIN
Query Match 37.0%; Score 94; DB 34; Length 538;
Best Local Similarity 74.6%; Pred. No. 3.23e-108;
Matches 150; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

DEFINITION m115c05_r1 Soares mouse p3NME19.5 Mus musculus EST mRNA clone
IMAGE:463594 5' similar to qb:U28486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION NID 9150070
VERSION VERSION EST
KEYWORDS EST
ORGANISM Mus musculus
SOURCE house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,N.
TITLE Unpublished (1995)
JOURNAL On May 18, 1995 this sequence version replaced gi:81026.
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:277410
Seq Primer: -28M13 rev2 from Amersham
High quality sequence stop: 469.
FEATURES source
1. .557
/organism="Mus musculus"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAACTGTAAGTGGGAGGCCGCCTTTTTTTT 3'], double stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minru Ko (Wayne State University)." /clone="IMAGE:349554" /clone_id="Soares mouse p3NME19.5" /dev_stage="19.5 dpc total fetus,"

Dr. Minoru Ko (Wayne State University)."
 /db_xref="taxon:10090"
 /map="5"
 /clone="IMAGE:45394"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"

BASE COUNT

143 a
155 c

148 g

111 t

ORIGIN

Query Match 37.0%; Score 94; DB 35; Length 557;
 Best Local Similarity 74.5%; Pred. No. 3.23e-108; Indels 0; Gaps 1;
 Matches 150; Conservative 0; Mismatches 50; Index 1;

Db 21 CCCAGCTAAGAGGGTTCCTGGCCACCTGTGTTGGCTGACTGTGTCGGAGG 80
 Qy 50 CCCAGACATGGAGGCTCCCTCCTGGCACAGCAGCTGGGGTGTGCTGGAGG 109

Db 81 CAGGGCACTCC-ACCACACCCAGGTCCTGCAAGCCAAGGCAAACATGTTCCCTG 139
 Qy 110 CAGGTGCGACTCCAGCACCCAGGTCCTACAGTGAAGTCAGTGCTGGCTCGAG 169

Db 140 AACAGAAACAGAGAGGTTGGATACTAGAGCCCTGGAGGCCCTGAAAGAAC 199
 Qy 170 AGCAGGACCCAGAGAACGGCTGGGGCCGGCTGGAGGACCTCCGGAGAAC 229

Db 200 AGCTGGGCCACTGTCTCTG 220
 Qy 230 AGCTGGGGCTGTCCTG 250

BASE COUNT

136 a
159 c

150 g

115 t

5 others

ORIGIN

Query Match 37.0%; Score 94; DB 34; Length 565;
 Best Local Similarity 74.5%; Pred. No. 3.23e-108; Indels 0; Gaps 1;
 Matches 150; Conservative 0; Mismatches 50; Index 1;

Db 48 CCCAGTATGAGGGTTCCTGGCCACCTGTGTTGGCTGCAAGCCTGGGGAGG 107
 Qy 50 CCCAGACAGGAGGCTCCCTGGTCACAGCCTGGTGTGCTGTGGAGG 109

Db 108 CAGGGCACTCC-ACCACACCCAGGTCCTGCAAGCCAAGGAAACATGTTCCCTG 166
 Qy 110 CAGGTGCGACTCCAGCACCCAGGTCCTACAGTGAAGTCAGTGCTGGCTCGAG 169

Db 167 AACAGAAACAGAGAGGTTGGATACTAGAGCCCTGGAGGCTCTGAAAGAAC 226
 Qy 170 AGCAGGACCCAGAGAGGCTGGGGGGGGCTGGAGGCCCTCCGGAGAAC 229

Db 227 AGCTGGGCCACTGTCTCTG 247
 Qy 230 AGCTGGGGCTGTCCTG 250

Search completed: Tue Aug 3 17:34:31 1999
 Job time : 709 secs.

RESULT 15 W35411 555 bp mRNA EST 11-SEP-1995
 DEFINITION mb3g11_r1 Soares mouse cDNA clone IMAGE:356058 5' similar to qb:U2486 Mus musculus uterine-specific
 proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION

W35411

NID

91318315

VERSION

W35411.1

KEYWORDS

EST

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

I (bases 1 to 555)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, R., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMM Mouse EST Project
 The WashU-HMM Mouse EST Project

TITLE

Unpublished (1995)

COMMENT
 On Nov 29, 1993 this sequence version replaced gi:430388.
 Contact: Marra M/Mouse EST Project

WashU-HMM Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 285 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:217468
 Seq. primer: ETPrimer
 High quality sequence stop: 361.

FEATURES

Source

1. .565

/organism="Mus musculus"

/note="Vector: pT7FD (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5' TGTACCAACTGAAAGGGAGGCCGCATTTTTTTTT 3'],"



FEATURES	
source	High quality sequence stop: 398. location/Qualifiers
1.	5.34 /organism="Homo sapiens" /note="Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization." /db_xref="taxon:9606" /clone="IMAGE:895032" /library_id="NCI_CGAP_CO3" /sex="pooled" /tissue_type="colon" /lab_host="DH10B"
BASE COUNT	80 a 160 c 178 g 115 t 1 others
ORIGIN	
Query Match	Best Local Similarity 83.3%; Score 512; DB 14; Length 534;
Matches	525; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db	2 CCGGGCCTGCTGGGTTATTCTAGTGGCAGGTAGGGAGGGTCCAGTCCAA 61 CCCGGCCTGCTGGGTTATTCTAGTGGCAGGTAGGGAGGGTCCAGTCCAA 554
Cp	62 CAGCTGGCCTGGGACAGGGGGGGAGTGATGGGCCCTGGAGGCCACTGGGTG 121 553 CACCTGGCCTGGGACAGGGGGGGAGTGATGGGCCCTGGAGGCCACTGGGTG 494
Db	122 GTAGATCTGGCTGGTTCTCCCTGGGAGGGGGGGAGTGATGGGCCCTGGAGGCCACTGGGTG 181 493 GTAGATCTGGCTGGTTCTCCCTGGGAGGGGGGGAGTGATGGGCCCTGGAGGCCACTGGGTG 434
Cp	182 CACGGGGCCTCCGGCTCTGGCTCTGGGTCTAGGGGAGGGGGAGACAGCTGCATG 241 433 CAACCGGGCCTCTCTGGCTCTGGGTCTCTGGGTCTAGGGGAGGGGGAGACAGCTGCATG 374
Db	242 GTGGGGCTGG3ACTCAAGAACGGGCCAGGGTGTCTCGTCATCCAGGCCCTGGT 373 GTGGGGCTGG3ACTCAAGAACGGGCCAGGGTGTCTCGTCATCCAGGCCCTGGT 301
Cp	302 GCCTGGAGGAAGGGCCCTGGCTGACCCGGCTCTCTGGGTCAAGATT 361 313 GCCTGGAGGAAGGGCCCTGGCTGACCCGGCTCTCTGGGTCAAGATT 254
Db	352 CGGGTCTGGGACAGAACGGGCCAGGGAGCTGGGTCTGGGTCAAGATT 254 253 CGGGTCTGGGACAGAACGGGCCAGGGAGCTGGGTCTGGGTCAAGATT 194
Cp	422 AGGGGGCCCCAGGC-TTCTCTGGGCTCTGGGTCAAGAGCCCTACTGGGTCAACCAC 480 193 AGGGGGCCCCAGGC-TTCTCTGGGCTCTGGGTCAAGAGCCCTACTGGGTCAACCAC 534
Db	481 GATAGGGAACTTGGTGTGGGATGACCTGGCTCTGGGTCAAGAGCCCTACTGGGTCAACCAC 134 133 GATAGGGACCTGGGCTGGACTGACCTGGCTCTGGGTCAAGAGCCCTACTGGGTCAACCAC 80
RESULT	2
OUCS	Aa568450 474 bp mRNA EST 09-SEP-1997
DEFINITION	similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA
SEQUENCE	
ACCESSION	Aa568450
ID	92341504
VERSION	Aa568450.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	
AUTHORS	Eutheria; Primates; Catarhini; Hominidae; Homo.
TITLE	(bases 1 to 474) http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) On Sep 12, 1996 this sequence version replaced gi:1402127.
CONTACT	Contact: Robert Strausberg, Ph.D.
CDNA LIBRARY PREPARATION	CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA SEQUENCING	DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution:	NCI_CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at: www-bio.lnl.gov/bbpr/image.html
Insert Length:	651 Std Error: 0.00
Seq primer:	46m13 fwd. Et from Amersham
High quality sequence stop:	197.
location/Qualifiers	
1.	474
/organism="Homo sapiens"	
/note="Organ: colon; Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)." /db_xref="taxon:9606" /clone="IMAGE:895032" /library_id="NCI_CGAP_CO10" /sex="colon_tumor RER+" /lab_host="DH10B"	
BASE COUNT	61 a 142 c 157 g 114 t
ORIGIN	
Query Match	Best Local Similarity 98.7%; Score 424; DB 15; Length 474;
Matches	455; Conservative 0; Mismatches 1; Indels 5; Gaps 5;
Db	16 TGCCGGCCCTGGGTATTCTGGTCAAGATT 74 615 TGCCGGCCCTGGGTATTCTGGTCAAGATT 556
Cp	75 AACACCTGGCCCTGGACAGGGGGGGAGTGATGGGCC-TGGAGGCC-TACTGGGTCAACCAC 133 555 AACACCTGGCCCTGGACAGGGGGGGAGTGATGGGCC-TGGAGGCC-TACTGGGTCAACCAC 496
Db	134 TTGTTAGATGGTGTGGCTCTCCGGTCCAGGACACCTGGTCAAGGGCTCTGGGTCAACCAC 193 495 TTGTTAGATGGTGTGGCTCTCCGGTCCAGGACACCTGGTCAAGGGCTCTGGGTCAACCAC 436
Cp	194 CACACCCGGCTCTCTGGCTCTGGGTCAAGGGCTCTGGGTCAACCAC 253 435 CACACCCGGCTCTCTGGCTCTGGGTCAAGGGCTCTGGGTCAACCAC 376
Db	254 TGGCTGGGCTGGGACTTGGACAGACGGGCCAGGGTCTCTGGCTCTGGCTCTGGGTCAAGGGCTCTGGGTCAACCAC 313 375 TGGCTGGGCTGGGACTTGGACAGACGGGCCAGGGTCTCTGGCTCTGGGTCAACCAC 436
Cp	314 TGGCTGGGACTTGGACAGACGGGCCAGGGTCTCTGGCTCTGGGTCAAGGGCTCTGGGTCAACCAC 373 315 GTCCTGGGAGGA-TGGGGCCCTGGCTGACCTC-GTGGCTCTCTC-GTGGGTCAAG 259 374 AGTTCCGCTCTGGGAGGGACAGCACCACTGGTCTCTGGGTCAACCAC 433

/dev_stage="20 week-post conception fetus"																								
BASE COUNT		89 a 119 c 133 g 75 t		119 c 133 g 75 t		8 others																		
ORIGIN		Query Match		50.2%		Score 309; DB 19;		Length 424;																
Best Local Similarity		92.0%		Pred. No. 0.00e+00;		0: Mismatches		23: Indels																
Matches		1390; Conservative		0:		Gaps		10;																
Db	1	CCAGAACATGAGGAGGGCTCTCTGGTACACGCCCTGGTGTGGTGGTGGTGGTGGTGGAGGC	Oy	43	CCGACAGTCAGGAGGGCTCTCTGGTACACGCCCTGGTGTGGTGGTGGTGGTGGTGGAGGC	60	60	102																
Db	61	AQGTGCACTCCAGCACCAAGTGCCTATCGAGATGCAAGTGCCTAGCCTGAGGAAACACTGGCCCTCAGA	Oy	103	AGGTGAGTCGCCAGCACCAAGTGCCTATCGAGATGCAAGTGCCTAGCAGTCAGTCAGTCAGCAACACTGGCCCTCAGA	120	162																	
Db	121	GCAAGGACCCAGAGAACGCTGG-CGCCCCTGGTGGTGGNGAGCCCTCGGAGAAGGAGGACCA	Oy	163	GCAAGGACCCAGAGAACGCTGGGCGCCGTTGGAGAAGGAGGACCA	179	222																	
Db	180	GCTGGGNTGCTGTCCTGTCAGAGGCCAACACTTGTACCGAGGAGGAGGACCG	Oy	223	GCTGGGNTGCTGTCAGAGGCCAACACTTGTACCGAGGAGGAGGACCG	239	282																	
Db	240	AGGTCAAGGGAGGGCCATTCCTCAGGGCACCAGGGTGATGGAGGAGGACAC	Oy	283	AGGTCAAGGGAGGGCCCATCTCTCAGGGCACCAGGGTGATGGAGGAGGACAC	299	342																	
Db	300	CCTGGGGCCGTCGTCCTGAGTTCGGAGCCGACATGACAGCTGGTGGAGGACAC	Oy	343	CCTGGG-CCTGTCCT-GAGT-CCCGAGCCGACCATGACAGCTGGT-ACCACTCCGC	359	398																	
Db	360	TGAGGAGGACAGGGTGCAGGTAGAGGCCCGTTTNGTGTATNCAAATCAAC	Oy	399	CTGAGGAGGA-CGAGG--CGAGG-AGAGGCCCGGTGTTGAT-GAT-GCCAAATCACC	419	452																	
Db	420	AGT 423	Oy	453	AGT 456																			
RESULT		5		LOCUS		EST		BASE COUNT																
DEFINITION	AA503839		501 bp mRNA		EST		62 a		148 c															
VERSION	AA503839.1		similar to TR:G899433 PROLINE-RICH ACIDIC PROTEIN.		EST		165 g		165 t															
COMMENT	On Apr 14, 1993 this sequence version replaced gi:693200.																							
REFERENCE	1 (bases 1 to 501)		Bukarvota; Metacoda; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.																					
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.																							
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index																							
JOURNAL	Unpublished (1997)																							
COMMENT	Contact: Robert Strausberg, Ph.D.																							
COMMENT	Tel: (301) 496-1550																							
COMMENT	Email: Robert.Strausberg@nih.gov																							
COMMENT	Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,																							
M. D.	Ph. D.																							
COMMENT	DNA Library Preparation: M. Bento Soares, Ph.D.																							
COMMENT	DNA Sequencing by: Washington University Genome Sequencing Center																							
COMMENT	Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbfrp/image/image.html																							
Insert Length: 586 Std Error: 0.00																								
Seq Primer: -40m13 fwd. ET from Amersham																								
High quality sequence stop: 190.																								
Location/Qualifiers																								
1. .501																								
/organism="Homo sapiens"																								
/note="Vector: pR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dt) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pR73 vector. Library went through one round of normalization."																								
/db_xref="Taxon:9606"																								
/clone="IMAGE:901050"																								
/clone.Lib="NCI-CGAP_Co3"																								
/sex="pooled"																								
/tissue.type="colon"																								
/lab.host="DH10B"																								
FEATURES																								
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SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
Eutheria; Primates; Catarrhini; Hominidae; Homo;	
REFERENCE	1 (bases 1 to 457)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., LeM., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 285 1800 Fax: 314 285 1810 Email: est@wuston.wustl.edu
LOCUS	7
DEFINITION	t85588.yd82910.rl soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:114786 5', mRNA sequence.
ACCESSION	T85588
NID	9713940
VERSION	17-MAR-1995
KEYWORDS	EST.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
Eutheria; Primates; Catarrhini; Hominidae; Homo;	
FEATURES	Insert Size: 671
SOURCE	High quality sequence stops: 210 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
BASE COUNT	Insert length: 671 Std Error: 0.00
ORIGIN	Seq primer: -21m13
FEATURES	High quality sequence stop: 210.
SOURCE	Location/Qualifiers
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/organism="Homo sapiens"	
/note="Organ: Liver and Spleen; Vector: pTR73D (Pharmacia)	
with a modified polylinker; Site-1: Pac I; Site-2: Eco RI;	
1st strand cDNA was primed with a Pac I - oligo(dT) primer	
[5' AACCTGGAGAATTATAAACGTTTAAAGCTTAAATTTTTTTT 3']	
double stranded cDNA was ligated to Eco RI adaptors	
(Pharmacia), digested with Pac I and cloned into the Pac I	
and Eco RI sites of the modified pTR73 vector. Library	
went through one round of normalization. Library	
constructed by Bento Soares and M.Fatima Bonaldo."	
/db_xref="taxon:9406"	
/clone=IMAGE:114786"	
/clone_lib="Soares fetal liver spleen INFSL"	
/sex="male"	
/dev_stage="20 week-post conception fetus"	
/lab_host="DH10B (ampicillin resistant)"	
73 a 146 g 106 t 11 others	
BASE COUNT	
ORIGIN	
FEATURES	
SOURCE	
Query Match	48.9%; Score 301; DB 19; Length 457;
Best Local Similarity	90.3%; Pred. No. 0.00e+00;
Matches	399; Conservative 0; Mismatches 30; Indels 13; Gaps 13;
Db	4 CCCGGCCTCGTGGCGTTATTGTGCTAGCTGGGN-AGGGTAGGGAGGGNCC-AGTCCCCA 61
Cp	513 CCCGGCCTGCIGGGITATTGTGCTAGCTGGGAGGGTAGGGAGGGTCCAGTCCCCA 554
Db	52 CAGCTGGGCCCTGGGACAGGGCGGGAGGTGAGGCCCTGGAGCCCTACTGGGGCG 121
Cp	553 CAGCTGGGCCCTGGGACAGGGCGGGAGGTGAGGCCCTGGAGCCCTACTGGGGCG 494
Db	122 GTAGATGTGGCTTGCTCTCGGTCAGGGACCTGGTATGGCATACCCA 181
Cp	493 GTAGATGTGGCTTGCTCTCGGTCAGGGACCTGGTATGGCATACCCA 434
Db	182 CAACGGGGCCTNTCTCGGCCCTGGTCTCTCAGGGCGAGGTGAGGCCCTGGAGCCCTACTGGGGCG 241
Cp	433 CAACGGGGCCTCTCGGCCCTGGTCTCTCAGGGCGAGGTGAGGCCCTGGAGCCCTACTGGGGCG 375
Db	242 GGTGGGNGTGGGANTCAGACAGGGNCCTCGGTNTCCATCCAGGCCTG 301
Cp	374 GTGCTGGCTGGGACTCAGACAGGGCTGGCTCTGGCTCATCCAGG-CCTG 316
Db	302 GTGCTGGAAAGGAATGGGGCCCTGCCTGACCTCGTGGCTCTCCCTGGCTCAA 361
RESULT	7
LOCUS	T85588
DEFINITION	351 bp mRNA
ACCESSION	T85588
NID	9713940
VERSION	17-MAR-1995
KEYWORDS	
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
Eutheria; Primates; Catarrhini; Hominidae; Homo;	
REFERENCE	1 (bases 1 to 351)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., LeM., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wuston.wustl.edu
LOCUS	7
DEFINITION	High quality sequence stops: 241 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
ACCESSION	Insert Length: 671 Std Error: 0.00
NID	Seq primer: M13RP1
VERSION	High quality sequence stops: 241 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
KEYWORDS	EST.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
Eutheria; Primates; Catarrhini; Hominidae; Homo;	
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SOURCE	High quality sequence stop: 241.
BASE COUNT	
ORIGIN	
FEATURES	
SOURCE	
1. .351	
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/note="Organ: Liver and Spleen; Vector: pTR73D (Pharmacia)	
with a modified polylinker; Site-1: Pac I; Site-2: Eco RI;	
1st strand cDNA was primed with a Pac I - oligo(dT) primer	
[5' AACCTGGAGAATTATAAACGTTTAAAGCTTAAATTTTTTTT 3']	
double stranded cDNA was ligated to Eco RI adaptors	
(Pharmacia), digested with Pac I and cloned into the Pac I	
and Eco RI sites of the modified pTR73 vector. Library	
went through one round of normalization. Library	
constructed by Bento Soares and M.Fatima Bonaldo."	
/db_xref="taxon:9403"	
/clone_xref="taxon:9605"	
/clone="IMAGE:114786"	
/clone_lib="Soares fetal liver spleen INFSL"	
/sex="male"	
/dev_stage="20 week-post conception fetus"	
/lab_host="DH10B (ampicillin resistant)"	
76 a 100 c 107 g 64 t 4 others	
BASE COUNT	
ORIGIN	
FEATURES	
SOURCE	
Query Match	46.8%; Score 288; DB 19; Length 351;
Best Local Similarity	95.2%; Pred. No. 0.00e+00;
Matches	316; Conservative 0; Mismatches 13; Indels 3; Gaps 3;
Db	5 GACATGAGGAGGCCTCTGGTCACCAAGCCCTGGTGTGCTGGGGAGGT 64

QY	47	GACATGAGGAGGCCTCTGTGTCACAGCCTGGTGTGCTGTTGGAGGAGGT	106	/note="Organ: uterus; vector: pBluescript SK; site_1: ECORI; Site_2: XbaI"
Db	65	GCAGTCCCAGCACCCAAAGTCCCTATCAAGATGCAAGTCAAACTGCCCCAG	124	/db_xref="NCBI (inhost):192971"
QY	107	GCAGTCCCAGCACCCAAAGTCCCTATCAAGATGCAAGTCAAACTGCCCCAG	124	/db_xref="taxon: 9606"
Db	125	GACCCAGAGAASGCCCTGGN-5CCGTTGGGGAGCTCCGAGAAGGACCGAG	183	/clone_id="uterus tumor I"
QY	167	GACCCAGAGAAGGCCCTGGGGCCGCTGGTGGAGGACCCAGCTG	166	/dev_stage="adult"
Db	184	GGGTGCGTGGTCTCTGTGAGGAGCCAAACTGTGACCACGGAGGAGCCACGGT	226	BASE COUNT 60 a 80 c 84 g 46 t 4 others
QY	227	GGGTGCGTGGTCTCTGTGAGGAGCCAAACTGTGACCACGGAGGAGCCACGGT	286	Query Match 43.3%; Score 266; DB 11; length 274;
Db	244	CAGGGCAAGGGCCATCTCTGAGGACCAAGGNTGGATGAGACCGACACTTG	303	Best local Similarity 97.8%; Pred. No. 0 00e+00;
QY	287	CAGGGCAAGGGCCATCTCTGAGGACCAAGGNTGGATGAGACCGACACTTG	346	Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
b	304	GGCTTTCCTTAAGTTCNTAGCCGACCAT 335		Db 1 CACTGCAGTCCTGAGCAGCTCTAGACATAGGAGGCTCT 60
Qy	347	GGCCGTCTCTGA-GTCCCAGGCCGACCAT 376		Qy 4 CACTGCAGTCCTGAGCAGCTCTAGACATAGGAGGCTCT 63
RESULT	8	AA299977		Db 61 CCTGGTACCCAGCCCTGGTGTGTCAGCTGGAGGAGGTGAGTCCAGGACCA 120
LOCUS		274 bp mRNA		Db 64 CCTGGTCACCCAGCTGGTGTGTCAGTCCAGCACCRA 123
DEFINITION		EST		Qy 121 GGTCTTATNAGATGCACTNAACACTGGCCCTCAGAGCAGGACCCAGAGGCTG 180
ACCESSION		AA299977		Qy 124 GGTCCCTACAAAGATGCACTAACACTGGCCCTCAGAGCAGGACCCAGGCTG 183
NID		91952328		Db 181 GGGGCCCTGGTGGAGACCTCCGGAGAGGAGGACAGCTGGGGCTGTGTCCT 240
VERSION		AA299977.1		Qy 184 GGGGCCCTGGTGGAGACCTCCGGAGAGGAGGACAGCTGGGGCTGTGTCCT 243
KEYWORDS		EST.		Db 241 CCAGAGCCAAACTTTGACCAACCGAGGAGAAG 274
SOURCE		Human.		Qy 244 CCAGAGCCAAACTTTGACCAACCGAGGAGAAG 277
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Primates; Catarrhini; Hominoidea; Homo. I (bases 1 to 274)		
AUTHORS		Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulndorff, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzzburgh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, J.-I., Marmeros, S.M., Merrick, J.M., Phillips, C.A., Spriggs, T.A., Utterback, T.R., Weidman, D.M., Shirley, R., Moreno-Palauques, R.F., McDonald, I.A., Nguyen, D.T., Pelliigrino, S.M., Small, K.V., Bednarik, D.P., Gao, L., Cepeda, M.A., Colenian, T.A., Collins, E.J., Dinkie, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., HungJung, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Rubin, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.		
TITLE		Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL		Nature 377 (6547 Suppl), 3-174 (1995)		
MEDLINE		956026280		
COMMENT		On Sep 12, 1996 this sequence version replaced gi:1394394.		
Other-ESTs:		THC104742		
Contact:		Kerlavage, AR		
Bioinformatics		The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
Location/Qualifiers		1..274		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
Location/Qualifiers		1..274		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
Location/Qualifiers		1..274		
FEATURES		source		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
Seq primer:		M13 Reverse		
Source		/organism="Homo sapiens"		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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Location/Qualifiers		1..274		
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Location/Qualifiers		1..274		
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Location/Qualifiers		1..274		
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)				
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(dev_stage="49 years old")

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BASE COUNT

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117 c

116 g

59 t

3 others

ORIGIN

Query Match

43.1%

Score 265;

DB 19;

Length 378;

Best Local Similarity

97.9%

Pred. No.

0.00e+00;

Matches

280;

Conservative

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Mismatches

4;

Indels

2;

Gaps

2;

Db

11

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59

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59

Oy

71

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Db

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Oy

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Db

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Oy

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Db

184

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185

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Db

186

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174

Oy

187

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174

Db

188

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Oy

189

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174

Db

190

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Oy

191

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Db

192

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Oy

193

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Db

194

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Oy

195

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174

Db

196

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Oy

197

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Db

198

TGGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

174

Oy

199

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174

Db

200

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174

Oy

201

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174

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174

/organism="Homo_sapiens"
 /note="Organ: Liver and Spleen; Vector: pRT73D (Pharmacia)
 with a modified Polylinker: Site_1: Pac I; Site_2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5', AATGGAGATAATTAAAGTCCTTITTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pRT3 vector. Library
 constructed by Bent Soares and M.Fattima Bonaldo."

/ab_xref="GDB:470308"
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 /clone.lib="Soares fetal liver spleen 1NFLS"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
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FEATURES

source

1. .357

High quality sequence stop:

232

Source:

IMAGE Consortium,

LNL

This clone is available royalty-free through LNL;

contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length:

716

Std Error:

0.00

Seq primer:

M13RP1

High quality sequence stop:

232

Location/Qualifiers

1. .357

TITLE Fraser,C.M. and Venter,J.C.
JOURNAL Initial assessment of human gene diversity and expression patterns
MEDLINE based upn 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

COMMENT On Apr 14, 1993 this sequence version replaced gi:837374.

Other ESTs: THCI04700
 Contact: Karlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018999056
 Fax: 301899423
 Email: arkarlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tgi/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES

SOURCE

1..188

/organism="Homo sapiens"
 /note="Orfani: epididymis; Vector: pBluescript SK-; Site_1:
 ECORI; Site_2: Xhol";
 /db_xref="NCICB:136917"
 /db_xref="taxon:9606"
 /clone_lib="Epididymus"
 /sex="male"
 /dev_stage="adult"
 /origin

40 a -68 c 51 g 26 t 3 others

BASE COUNT

Query Match: 29.9%; Score: 184; DB 11; Length: 188;
 Best Local Similarity: 98.4%; Pred. No. 1 67e-260; Matches: 0; Mismatches: 3; Indels: 0; Gaps: 0;

Db 2 CCGGTNTTGGTAGGCCAATNACAGGTCTGGGACGGGAGGAAGAACRAGACCA 61
 Qy 427 CCGGTGTGGGTGATGCCAATCACCAGGTCTCTGGACGGGAGGAAGACCAAGACCA 486

Db 62 CATCTACACCCCGTAGGCCCTCAGGGCCATGACTGCCCGCCGCCCCCTGTCAGGCC 121
 Qy 487 CATCTACACCCCGTAGGCCCTCAGGGCCATGACTGCCCGCCGCCCCCTGTCAGGCC 546

Db 122 CAGGTGTGGGACTGGACCCCTCCTACCTGCCCAGCTACAACTAAACCNACCA 181
 Qy 547 CAGCTGTGGGACTGGACCCCTCCTACCTGCCCAGCTACAACTAAACCCAGCA 606

Db 182 GGCGGG 188
 Qy 607 GGCGGG 613

BASE COUNT

Query Match: 22.6%; Score: 139; DB 14; Length: 139;
 Best Local Similarity: 100.0%; Pred. No. 6.24e-183; Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

ORIGIN

42 a -42 c 47 g 33 t

BASE COUNT

Query Match: 22.6%; Score: 139; DB 14; Length: 139;
 Best Local Similarity: 100.0%; Pred. No. 6.24e-183; Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

ORIGIN

42 a -42 c 47 g 33 t

FEATURES

SOURCE

1..139

/organism="Homo sapiens"
 /note="Vector: pTRT3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTRT3 vector. Library went through one round of normalization."
 /db_xref="taxon:9606"
 /clone_id="IMAGE:92144"
 /clone_lib="NCI_CGAP_C03"
 /sex="pooled"
 /tissue_type="colon"
 /lab_host="DH10B"

BASE COUNT

Query Match: 22.6%; Score: 139; DB 14; Length: 139;
 Best Local Similarity: 100.0%; Pred. No. 6.24e-183; Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

ORIGIN

42 a -42 c 47 g 33 t

BASE COUNT

Query Match: 22.6%; Score: 139; DB 14; Length: 139;
 Best Local Similarity: 100.0%; Pred. No. 6.24e-183; Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

ORIGIN

42 a -42 c 47 g 33 t

RESULT

12

LOCUS A551860 139 bp mRNA EST 04-SEP-1997

DEFINITION n901c09.s1 NCI_CGAP_C03 Homo sapiens cdna clone IMAGE:28144 3'

Similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ; mRNA sequence.

ACCESSION AA551860

NID 9232212

VERSION A551860.1

KEYWORDS EST.

SOURCE

human.

ORGANISM Homo sapiens

RESULT

13

LOCUS A1391147 560 bp mRNA EST 02-FEB-1999

DEFINITION mc16001_Y1_Soares mouse P3NNM19.5 Mus musculus cDNA clone IMAGE:348720 5' similar to qb:U22486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION A1391147

NID 9421754

VERSION A1391147.1

KEYWORDS EST.

SOURCE

house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 139)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stoeckle,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,I., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

JOURNAL The WashU-NCI Mouse EST Project 1999

COMMENT Unpublished (1997)

On Apr 14, 1993 this sequence version replaced gi:838020.

Contact: Robert Strausberg, Ph.D.

RESULT

13

LOCUS A1391147 560 bp mRNA EST 02-FEB-1999

DEFINITION mc16001_Y1_Soares mouse P3NNM19.5 Mus musculus cDNA clone IMAGE:348720 5' similar to qb:U22486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION A1391147

NID 9421754

VERSION A1391147.1

KEYWORDS EST.

SOURCE

house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Mus. (bases 1 to 560)

REFERENCE Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stoeckle,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,I., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stoeckle,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,I., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

JOURNAL The WashU-NCI Mouse EST Project 1999

COMMENT Unpublished (1999)

COMMENT

On Apr 14, 1993 this sequence version replaced gi:716760.

Contact:

Marra MaWashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone

(correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 4865.

FEATURES

SOURCE

1. -560

/organism="Mus musculus"

/note="vector: pT73D (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dt) primer [5',

TGTTACCAATCTGAAGTGCGGCCGCAATTTCCTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Dr. Minoru Ko (Wayne State University).

{db_xref="taxon:10090"

/map="12"

/clone="IMAGE:348720"

{clone.lib="Soares mouse p3NMF19.5"

{dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"

BASE COUNT

136 a
152 c
148 g
113 t
1 others

ORIGIN

Query Match 16.7%; Score 103; DB 26; Length 560;

Best Local Similarity 71.7%; Pred. No. 2.71e-122; Mismatches 0; Indels 0; Gaps 0;

Matches 170; Conservative 0; Polymorphic 0; Insertions 0; Deletions 0;

Db 44 CCCAGTCATGAGGAGGTTCCTGGCCACCTGTTGGTGCAGCTGCTGGAGG 103

Qy 42 CCCAGACATGAGGAGGTCTCTGGTACCCAGCTGGAGG 101

Db 104 CAGGGCAGCTCCAGCACCCAGGCTCTGTCAAGACAAAGGGAAACTGTGTCCTG 163

Qy 102 CAGGTGAGTCGCCAGCACCAAGGTCTATCAGATGCAAGTCACACTGCCCTCAG 161

Db 154 AACAGAACAGAGAACGGCTGATACTAGAGCCCTCTGGAAAGACAACC 223

Qy 162 AGGAGGACCAAGAGAGGCCGCGCCGGTGGTGGAGGCC 221

Db 224 AGCTGGGCCACTCTCTCTGAACCAAACAGAACAGCCCTGCAAGCTGCCAGGAAAGC 280

Qy 222 AGCTGGTGTGCTGTCAGAACGCCAAACTCTTGACCAACCGAGGAGGC 278

BASE COUNT

152 a
176 c
151 g
118 t
2 others

ORIGIN

Query Match 16.7%; Score 103; DB 25; Length 590;

Best Local Similarity 71.7%; Pred. No. 2.71e-122; Mismatches 0; Indels 0; Gaps 0;

Matches 170; Conservative 0; Polymorphic 0; Insertions 0; Deletions 0;

Db 45 CCCAGTCATGAGGAGGTCTCTGGCCACCTGTTGGTGCCTGGTGGAGG 105

Qy 42 CCCAGACATGAGGAGGTCTCTGGTACCCAGCTGGAGG 101

Db 106 CAGGGCAGCTCCAGCACCCAGCTGGTCTGGAGGACCAACATGTTCTG 165

Qy 102 CAGGTGAGTCGCCAGCACCAAGGTCTATCAGATGCAAGTCACACTGCCCTCAG 161

Db 166 AACAGAACAGAGAACGGCTGAGATACTAGAGCCCTGAGGAGGACCC 225

Qy 162 AGCAGGACCAAGAGAACGCCCTGGGGCCCCGGTGGGGAGGAGGACCC 221

Db 226 AGCTGGGCCACTCTCTCTGAACCAAACAGAACAGCCACTGTGCAAGTCAACACTGCCCTCAG 161

Qy 222 AGCTGGTGTGCTGTCAGAACGCCAAACTCTTGACCAACCGAGGAGGC 278

RESULT 15 W36494 578 bp mRNA EST 11-SEP-1996

DEFINITION mb71h0.r1 Soares mouse p3NMF19.5 mus musculus cDNA clone

IMAGE:334915 5' similar to gb:U28486 mus musculus uterine-specific

proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION A1323091

VERSION 94057520

VERSION A1323091.1 GI:4057520

KEYWORDS EST, house mouse.

SOURCE Eutheria: Rodentia: Sciurognathii: Muridae: Murinae: Mus.

REFERENCE

1 (bases 1 to 590)

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubroque,T., Geisel,S., Kucaba,T., Lucy,M., LeM.N., Martin,J.J., Morris,M., Scheibenbogen,K., Stoeptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE

The WashU-HMM Mouse EST Project

JOURNAL

Unpublished (1996)

On Apr 14, 1993 this sequence version replaced gi:693536.

COMMENT

Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone

(correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 444.

FEATURES

SOURCE

1. -590

/organism="Mus musculus"

/note="vector: pT73D (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dt) primer [5',

TGTTACCAATCTGAAGTGCGGCCGCAATTTCCTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M. Fatima Bonaldo. RNA was kindly provided by

Dr. Minoru Ko (Wayne State University)."

{db_xref="taxon:10090"

/map="between DIS1165 and UGB"

{clone.lib="IMAGE:481715"

{clone.lib="Soares mouse p3NMF19.5"

{dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"

BASE COUNT

152 a
176 c
151 g
118 t
2 others

ORIGIN

Query Match 16.7%; Score 103; DB 25; Length 590;

Best Local Similarity 71.7%; Pred. No. 2.71e-122; Mismatches 0; Indels 0; Gaps 0;

Matches 170; Conservative 0; Polymorphic 0; Insertions 0; Deletions 0;

Db 45 CCCAGTCATGAGGAGGTCTCTGGCCACCTGTTGGTGCCTGGTGGAGG 105

Qy 42 CCCAGACATGAGGAGGTCTCTGGTACCCAGCTGGAGG 101

Db 106 CAGGGCAGCTCCAGCACCCAGCTGGTCTGGAGGACCAACATGTTCTG 165

Qy 102 CAGGTGAGTCGCCAGCACCAAGGTCTATCAGATGCAAGTCACACTGCCCTCAG 161

Db 166 AACAGAACAGAGAACGGCTGAGATACTAGAGCCCTGAGGACCC 225

Qy 162 AGCAGGACCAAGAGAACGCCCTGGGGCCCCGGTGGGGAGGACCC 221

Db 226 AGCTGGGCCACTCTCTCTGAACCAAACAGAACAGCCACTGTGCAAGTCAACACTGCCCTCAG 161

Qy 222 AGCTGGTGTGCTGTCAGAACGCCAAACTCTTGACCAACCGAGGAGGC 278

RESULT 15 W36494 578 bp mRNA EST 11-SEP-1996

DEFINITION mb71h0.r1 Soares mouse p3NMF19.5 mus musculus cDNA clone

IMAGE:334915 5' similar to gb:U28486 mus musculus uterine-specific

proline-rich acidic protein (MOUSE); mRNA sequence.

ACCESSION A1323091

VERSION 94057520

VERSION A1323091.1 GI:4057520

KEYWORDS EST, house mouse.

SOURCE Eutheria: Rodentia: Sciurognathii: Muridae: Murinae: Mus.

REFERENCE

1 (bases 1 to 590)

Search completed: Tue Aug 3 19:16:07 1999
Job time : 1353 secs.

ACCESSION W36494
NID 91318399
VERSION W36494.1 GI:1318399
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 578)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Scheibenbogen,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,N.
TITLE The WashU-HMM Mouse EST Project
COMMENT Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430545.
Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty free through LILN ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: BTPrimer
high quality sequence stop: 401.
FEATURES location/Qualifiers
source
1. . 578
/organism="Mus musculus"
/note="vector: pMT3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(d) primer [5',
TGTATCCCATCTCGAAGTGGCGCAATTGTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
(Pharmacia). Library went through one round of
normalization to a COT = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090",
/map="31",
/clone="IMGE:334915"
/clone_id="Soares mouse pJNMF19.5"
/dev_stage="19.5 dpc total fetus",
/lab_host="DH10B (ampicillin resistant)"
/map="31",
/clone="IMGE:334915"
/dev_stage="19.5 dpc total fetus",
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 143 a . 155 c . 159 g . 114 t . 7 others
ORIGIN

Query Match
Best Local Similarity 16.3%; Score 100; DB 34; Length 578;
Matches 171; Conservative 0; Mismatches 65; Indels 1; Gaps 1;
Db 44 CCCAGTCATGAGAGGTTCTCTGCGACTGCTGAGG 103
Qy 42 CCCAGAGATGGAGGCTCTCTGGTACAGCCCTGGTGGAGG 101
Db 104 CAGGCCAGTCC-AGCACACAGGCTCTGTGAGACCAACATGTGTCCTG 162
Qy 102 CAGTGAGTCAGCACCAGTGCTCATGAGATGCAAGTCAAACACTGGCCTCAG 161
Db 163 AACAGAAACAGAGAGCTGGATACTAGAGCCCTGGACCTCTGAAAGGACAAC 222
Qy 162 AGCAGGACCCAGAGGAAGGGCTGGGGGCCCTGGTGGAGCCTCGGGAGAAC 221
Db 223 AGCTGGGCACTGCTCTGCAACCAACAGAGAAGGAGCTGGAGCTCCGAGGAGC 279
Qy 222 AGCTGGGCACTGCTCTGCAACCAACAGAGAAGGAGCTGGAGCTCCGAGGAGC 279